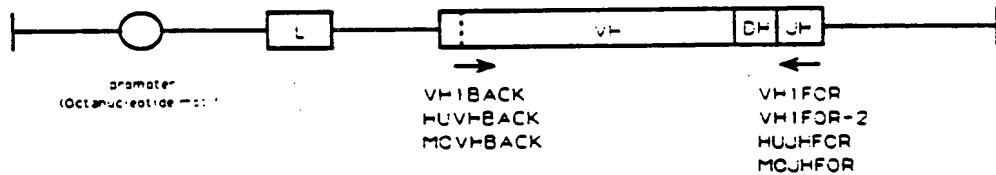


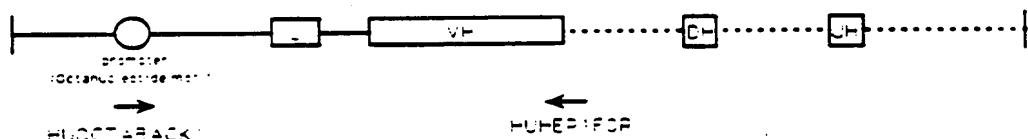
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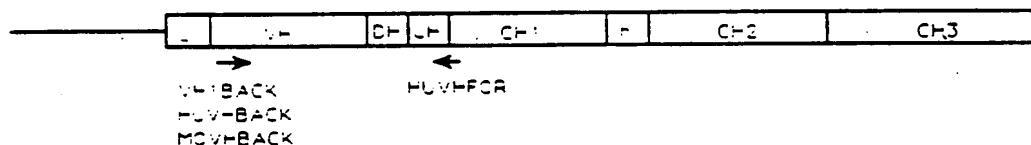
Rearranged heavy chain variable gene (DNA):



Unrearranged heavy chain variable gene (DNA):



Rearranged heavy chain variable gene (mRNA):



Rearranged light chain variable gene (DNA):

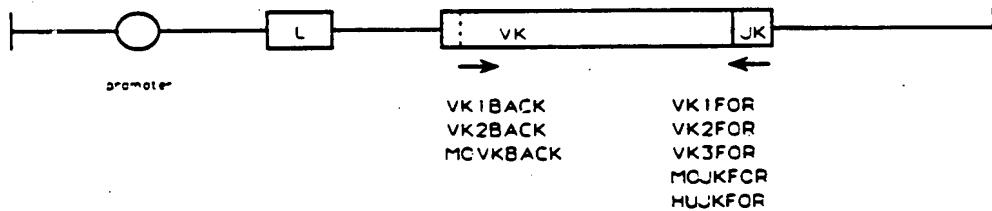


FIG. 1

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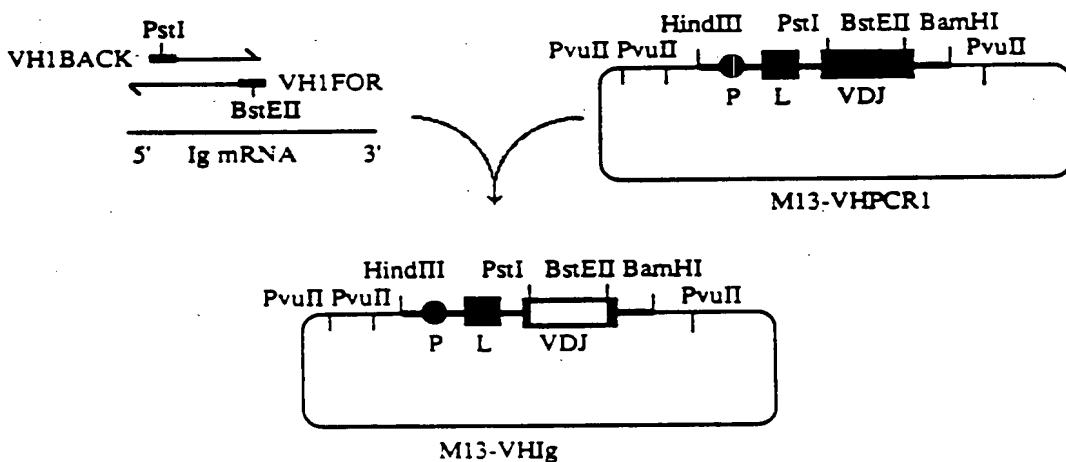


FIG. 2

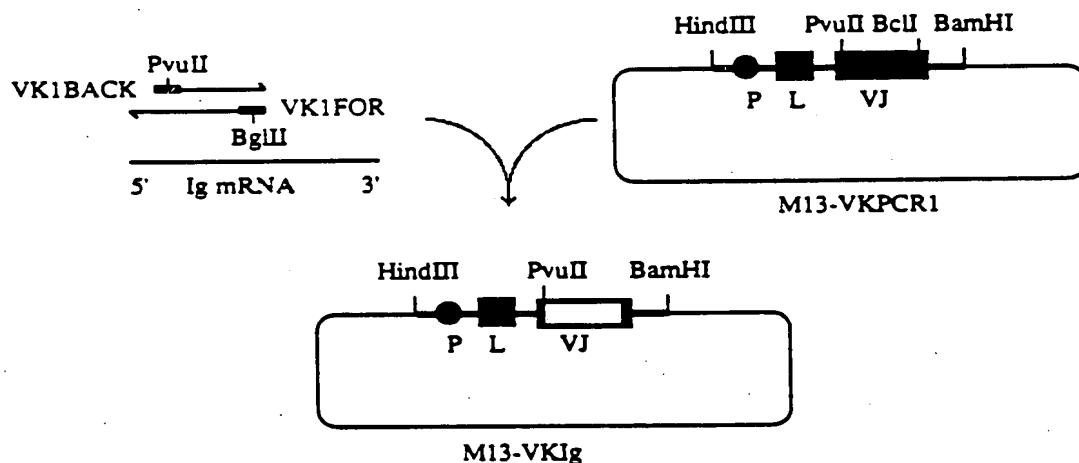


FIG. 4

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ML3 VHPCR1.

HIND III^a

AAGCTTATGAATATGCAAATCCTCTGAATCTACATGGTAAATATAGGTTTGTCTATACCA
10 20 30 40 50 60

CAACAGAAAAACATGAGATCACAGTTCTCTACAGTTACTGAGCACACAGGACCTCAC
70 80 90 100 110 120

M G W S C I I L F L V A T A T
CATGGGATGGAGCTGATCATCCTCTCTGGTAGCAACRGCTACAGGTAAAGGGGCTCAC
130 140 150 160 170 180

AGTAGCAGGCTTGAGGTCTGGACATATATATGGGTGACAATGACATCCACTTGCCTTC
190 200 210 220 230 240

PstI

G V H S Q V Q L Q E S G P G L V R P
1 51 10
TCTGCACAGGTGTCAGTCCAGGTCAGCTGAGGAGCCGGTCCAGGTCTTGAGAC
250 260 270 280 290 300

CDR1

S Q T L S L T C T V S G S T F S S Y W M
15 20 25 30
CTAGCCAGACCCGTGAGCTGACCTGACCGGTGCTGGCACACCTTCAGCAGCTACTGGA
310 320 330 340 350 360

CDR2

H W V R Q P P G R G L E W I G R I D P N
35 40 45 50
TGCACGGGTGAGACAGCCACCTGGACGGTCTTGAGTGGATTGGAAGGATTGATCTA
370 380 390 400 410 420

S G G T K Y N E K F K S R V T M L V D T
55 60 65 70
ATAGGGTGGTACTAACTACATGAGAAGTCAAGAGGAGAGTGACAATGCTGGTAGACA
430 440 450 460 470 480

S K N Q F S L R L S S V T A A D T A V Y
75 80 85 90
CCAGCAAGAACCACTTCAGCCTGAGACCTAGCAGCGTGACAGCCGCCACACCGCGGTCT
490 500 510 520 530 540

CDR3

Y C A R Y D Y Y G S S Y F D Y W G Q G T
95 100 105 110
ATTATGTGCAAGATACCAATTACTACGGTAGTAGCTCTTGACTACTGGGCCAAGGGA
550 560 570 580 590 600

BstEII

T V T V S S
115 120
CCACGGTACCGTCTCTCAGGTGAGTCCTACACCTCTCTCTTCTATTCAAGCTAAAT
610 620 630 640 650 660

AGATTTACTGCATTGGGGGGAAATGTGTGTATCTGAATTTCAGGTATGAAGGA
670 680 690 700 710 720

CTAGGGACACCTGGGACTCAGAAAGGGTCATTGGGAGCCCGGGCTGATGCAGACAGACA
730 740 750 760 770 780

BamHI

TCCTCAGCTCCAGACTTCATGGCCAGAGATTATAG
790 800 810

FIG. 3

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ML3 V_kPCRI

Hand III

AAGCTATGAAATATGAAA T C C T G A A T T A C A G G T A A A T A C A G G T T G T G T A T A C C A
38 48 58 68 78 88

C A A C A G A A A A C A T G A G A T C A C A G T T C T G T C A C A G T T A C T G A G G A C A C A G G A C C T C A C
98 108 118 128 138 148

M G W S C I I L F L V A T A T
C A T G G G A T G G G A G C T G T A T C A T C T C T C T G T G A C A A C A G C T A C A G G T A A G G G G C T C A C
158 168 178 188 198 208

A G T A G C A G G S T T G A G G T C T G G A C A T A C A T G G G T G A C A T G A C A T C C A C T T G C C T T C
218 228 238 248 258 268

Hand II

G V H S D I C I S O S P S S L S A S 10
T C T C C A C A G G T G T C C A C T C C G A C A T C S A S S C C A G G C C A A G C A G G C C T G A G G C C A
278 288 298 308 318 328

CDR1

15 20 25 30
V G D R V T I T C R A S G N I H N Y L A
G C G T G G G T G A C A G A G T G A C C A T G A C T G T G A G G C C A G G C G T A R C A T C C A C A C T A C C T G G
338 348 358 368 378 388

CDR2

35 40 45 50
W Y Q Q K P G K A P K L L I Y Y T T T L
C T T G G T A C C A S C A G A A G C C A G G T A A G G C T C S A A A G C T G C T G A T C T A C T A C A C C A C C A C C
398 408 418 428 438 448

55 60 65 70
A D G V P S R F S G S G S G T D F T F T
T G G C T G A C G G T G T G C C A A G C A T T C A G C G G T A G C G G T A C C G A C T T C A C C T C A
458 468 478 488 498 508

CDR3

75 80 85 90
I S S L Q P E D I A T Y Y C Q H F W S T
C C A T C A G C A G C C T C C A G C C A G A G G A C A T C G C C A C C T A C T A C T G C C A G C A C T T C T G G A G C A
518 528 538 548 558 568

Bcl I (requires dam⁻ host)

95 100 105 108
P R T F G Q G T K V V I K R
C C C C A A G G A C S T T C G G C A A G G G A C C A A G G T G G T G A C T G A C T G A C T G A G T A G A A T T T A A C T
578 588 598 608 618 628

BamHI

T T G C T T C C T C A G T T G C C A C C
638 648

FIG. 5

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Sequence of MBrl VH

Splice -1
↓ G V H S
AGGTGTCCACTCC
20
1 PstI 10
Q V Q L Q E S G T E L A S P G A S V T L
CAGGACCACTACATGAGCTGAGCTGAGCTGGCGAGTCCTGGGGCATCAGTGACACTG
VH1BACK SITE
30 CDR1 40
S C K A S G Y T F T D H I N W V K K R
TCCTGCAAGGGCTTGCGCTACACATTACTGACCATATTAAATTGGGTAAGGGAGGG
52a 53 CDR2
P G Q G L E W I G R I Y P V S G V I N Y
CCTGGACAGGGCTTGAGTGGATTGGAGGAATTATCCAGTAAGTGGTGTAACTAAC
60 CDR2 65 70
N C K F M E K A T F S V D R S S N T V Y
AATCRAAAATTCACTGGCAAGGGCCTGAGCTGAGCCGTCCTCCACACAGTGAC
80 82A B C 83 90 CDR3
M V L N S I T S E D P A V Y Y C G R G F
ATGGTGGTGAACATCTGAGGACCTGCTGTCTATTACTGTGGAAAGGGGCTT
67 CDR3 83 BstEII Splice
D F D Y W G Q G T T V I T V S S ↓
GATTTGACTACTGGGCAAGGGACACGGTACCGCTCTCAGGT.....
VH1FOR SITE

Sequence of MBrl VK

Splice -1
↓ G V H S
AGGTGTCCACTCC
20
1 Pvull 10
D I Q I T Q S P P S L T V S V G E R V T
GACATGAGCTGAGCTGAGCTGAGCTGACTGTGTCACTAGGAGAGAGGGTCACT
VH1BACK SITE
27A B C D E F CDR1
I S C K S N O N I L W S G N R R Y C L G
ATCAGTTGCAAACTCCGATCAGAACCTTATGGAGTGGAACCGAAGGTACTGTTGGC
35 40 50 CDR2
W H Q W K P G Q T P T P L I T W T S D R
TGGCACCAGTGGAAACCGGGCAAACCTCCACACCGTGTACCTGGACATCTGATAGG
60 65 70
F S G V P D R F I G S G S V T D F T L T
TTCTCTGGAGTCCCTGATCTGTTCTAGGCAGTGGATCTGTGACAGATTCACTCTGACC
80 85 90 CDR3
I S S V Q A E D V A V Y F C Q Q H L D L
ATCAGCAGTGTGAGCTGAAGATGTGGCAGTTATTTCTGTCAGCAACATTTGGACCTT
95 100 BglII/BclI Splice
P Y T I F G G G T K L E I K ↓
CCGTACACGTTGGAGGGGGACCAAGCTGGAGATCAAACGTGAG
VH1FOR SITE

FIG. 6

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α -Lys 30

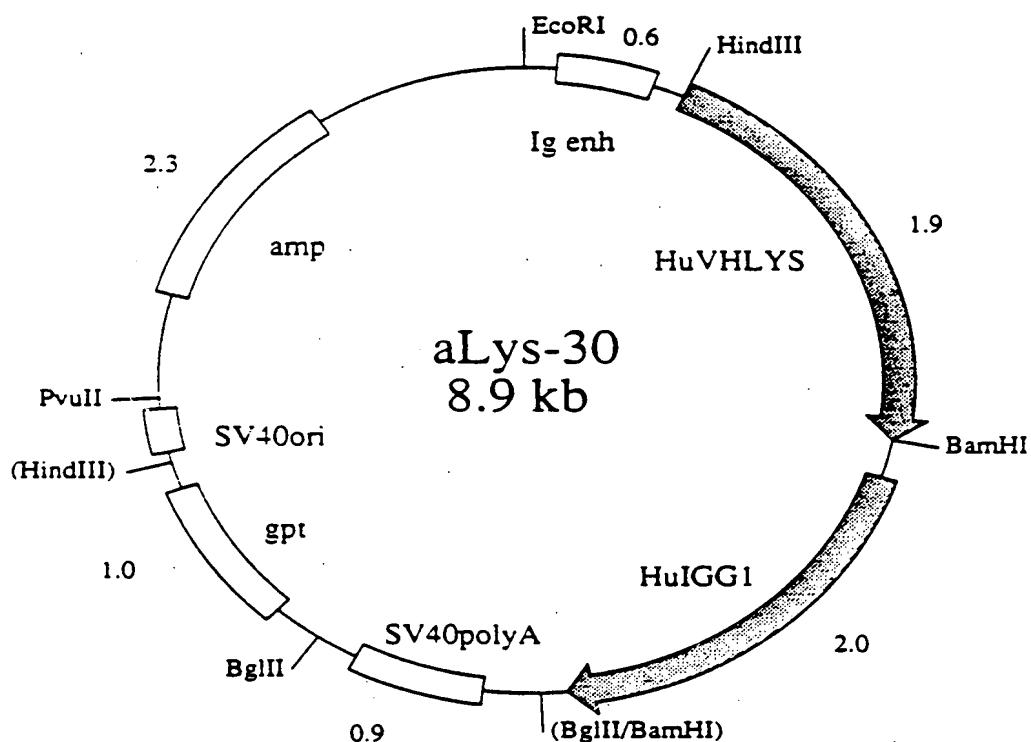


FIG. 7

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α -Lys 17

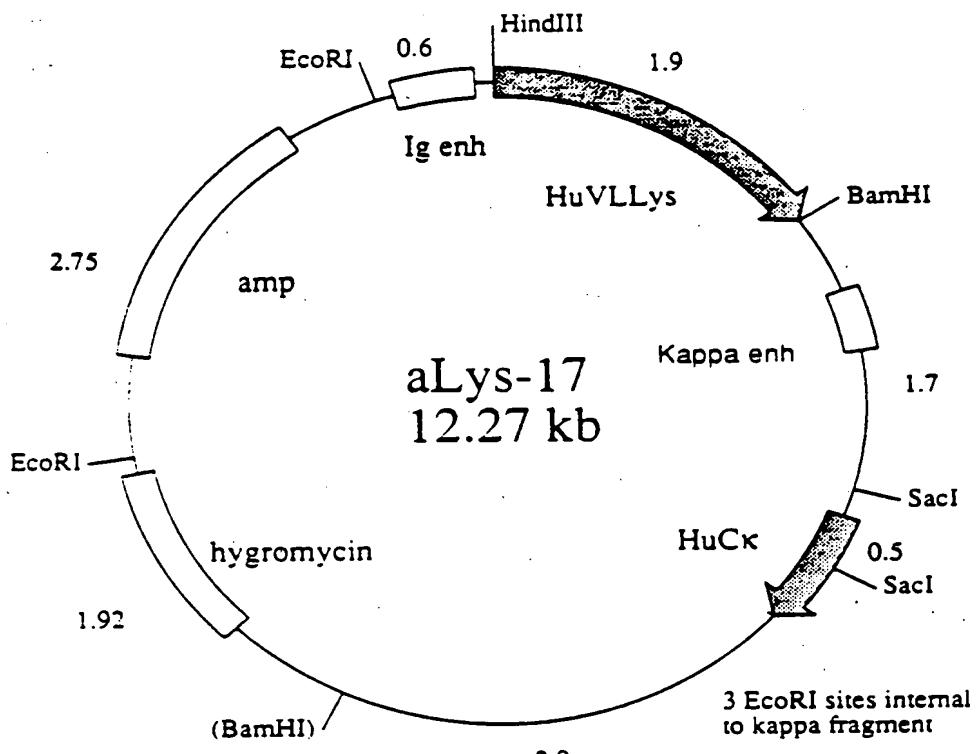
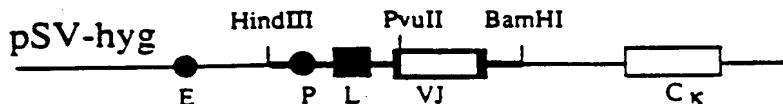


FIG. 8



FIG. 9



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ER1

CDR 1

ER2

CDR 2

KABAT IA

AC7	PGLVCPGSQSLSLTCSVTGYSIT	SYMM	WVRCPGPKALEWIG	YISYDGSSNNYNPFLKN
AC9	PGLVCPGSQSLSLTCSVTGFFIT	SYMM	WVRCPGPKALEWIG	YITHSGETTYNFSLCS
EC3	PGLVCPGSQSLSLTCSVTGYSIT	SYMM	WVRCPGPKALEWIG	YISYDGSSNNYNPFLKN
GC1	PGLVCPGSQSLSLTCSVTGYSIT	SYMM	WVRCPGPKALEWIG	YISYDGSSNNYNPFLKN

KABAT IB

AC6	PGLVCPGSQSLSLTCSVTGFSIT	SYGL	WVRCPGPKALEWIG	VIHAGGJTNYNSALMS
25G07	PGLVCPGSQSLSLTCSVTGFSIT	SYGL	WVRCPGPKALEWIG	VIWSGGSTDYNAAFIS
BC3	PGLVCPGSQSLSLTCSVTGFSIT	SYGL	WVRCPGPKALEWIG	VIHGGGSTDYNSALMS
GC3	PGLVCPGSQSLSLTCSVTGFSIT	SYGL	WVRCPGPKALEWIG	VIHAGGJTNYNSALMS
HC9	PGLVCPGSQSLSLTCSVTGFSIT	SYGL	WVRCPGPKALEWIG	VIHAGGJTNYNSALMS
25G10	PGLVCPGSQSLSLTCSVTGFSIT	SYAL	WVRCPGPKALEWIG	VIHGGGSTDYNSALKS
AL2	PGLVCPGSQSLSLTCSVTGFSIT	SYAL	WVRCPGPKALEWIG	VIHGGGSTDYNSALKS
AC8	PGLVCPGSQSLSLTCSVTGFSIT	SYGL	WVRCPGPKALEWIG**	*****GSTTJNSALKS
25G08	PGLVCPGSQSLSLTCSVTGFSIT	SYDV	WVRCPGPKALEWIG	VIHGGGSTDYNSALKS
AC3	PGLVCPGSQSLSLTCSVTGFSIT	SYGL	WVRCPGPKALEWIG	VIHAGGJTNYNAAFIS
CC7	PGLVCPGSQSLSLTCSVTGFSIT	SYGL	WVRCPGPKALEWIG	VIHAGGJTNYNSALMS
HC4	PGLVCPGSQSLSLTCSVTGFSIT	SYGL	WVRCPGPKALEWIG	VIHAGGJTNYNSALMS

KABAT IIA

EC4	PGLVCPGSVTKLSCSKASGYFFF	SYAMH	WVKCPSHAKSLEWIG	VISTYYGDASYNQFKG
HC7	PGLVCPGSVTKLSCSKASGYFFF	SYAMH	WVKCPSHAKSLEWIG	VISTYYGDASYNQFKG

KABAT IIB

AC2	ABLVCPGASVTKLSCSKASGYFFF	SYAMH	WVKCRPGGLEWIG	EIDPSDSYTNYNEKFKG
BC4	ABLVCPGASVTKLSCSKASGYFFF	SYWLT	WVKCRPGGLEWIG	DIYPGSGSTTNYNEKFKS
CC6	ABLVCPGASVTKLSCSKASGYFFF	SYAMH	WVKCRPGGLEWIG	RIDPSGSGGTJYNEKFKS
DC9	ABLVCPGASVTKLSCSKASGYFFF	SYAMH	WVKCRPGGLEWIG	EINPSNGGTNYDEKFKS
EC6	ABLVCPGASVTKLSCSKASGYFFF	SYWLT	WVKCRPGGLEWIG	DIYPGSGSTTNYNEKFKS
GC9	ABLVCPGASVTKLSCSKASGYFFF	SYAMH	WVKCRPGGLEWIG	EINPSNGGTNYNEKFKS
HC1	ABLVCPGASVTKLSCSKASGYFFF	SYAMH	WVKCRPGGLEWIG	ACDPETGGTAYNQFKG
GC8	PELVCPGASVTKLSCSKASGYFFF	SYAMH	WVKCRPGGLEWIG	WIYPGSGNTJYNEKFKG
HC1	ABLVCPGASVTKLSCSKASGYFFF	SYAMH	WVKCRPGGLEWIG	RIDPSDSDTNYNEKFKG
25G19	ABLVCPGASVTKLSCSKASGYFFF	SYPLS	WVKCNSHAKSLEWIG	NFHPYNDOTJYNEKFKG
FC4	TELVCPGASVTKLSCSKASGYFFF	SYAMH	WVKCRPGGLEWIG	NINPSNGGTNYNEKFKG
HC2	ABLVCPGASVTKLSCSKASGYFFF	SYAMH	WVKCRPGGLEWIG	NIDPSDSETHYNEKFKG
HC1	ABLVCPGASVTKLSCSKASGYFFF	SYAMH	WVKCRPGGLEWIG	EIDPSDSYTNY-KVCG
25G05	PELVCPGASVTKLSCSKASGYFFF	SYWLT	WVKCRPGGLEWIG	QIFPPASGSTYYNEHFKD
BC1	ABLVCPGASVTKLSCSKASGYFFF	SYWLT	WVKCRPGGLEWIG	DIYPGSGSTTNYNEKFKS
BC1	ABLVCPGASVTKLSCSKASGYFFF	RGAMH	WVKCRPGGLEWIG	SFTMYSDATEYSENFKG
HC1	ABLVCPGASVTKLSCSKASGYFFF	SYWLT	WVKCRPGGLEWIG	DIYPGSGSTTNYNEKFKS

KABAT III A

25G03	GOLVCPGSLSLSCAAASOFTFS	SYMM	WVRCPGPKALEWIG	EIRNKANGYTYEYASAVKG
BC1	GOLVCPGSLSLSCAAASOFTFS	SYMM	WVRCPGPKALEWIG	EIRNKANGYTYEYASAVKG
BC1	GOLVCPGSLSLSCAAASOFTFS	SYMM	WVRCPGPKALEWIG	EIRNKANGYTYEYASAVKG

KABAT III B

CC5	GOLVCPGSLSLSCAAASOFTFS	SYMM	WVRCPGPKALEWIG	YISSGSESTYYADTVKG
BL2	GOLVCPGSLSLSCESNEYFFF	SHDMS	WV*****VA	AINSDGGSTYYPDTMF
CC4	GOLVCPGSLSLSCAAASOFTFS	SYAMS	WVA*APGKOLEWIG	AISGSGGSTYYADSVKG
CC5	GOLVCPGSLSLSCAAASOFTFS	SYAMS	WVA*APGKOLEWIG	AISGSGGSTYYADSVKG
FL2	GOLVCPGSLSLSCESNEYFFF	*****	WVCP*PERLEVA	AINSDGGSTYYPDTMF
FC6	GOLVCPGSLSLSCAAASOFTFS	SYAMS	WVA*APGKOLEWIG	AISGSGGSTYYADSAKG
CC2	GOLVCPGSLSLSCESNEYFFF	*HDMS	WVRQDSSE*LEVA	AINSDGGSTYYPDTMF
FC9	GOLVCPGSLSLSCAAASOFTFS	SYGLS	WVRQDSSE*LEVA	TISSQGSSTYYPDSVKG

KABAT III C

EC6	GOLVCPGSLSLSCAAASOFTFS	DAWMS	WVRQDSPEKOLEWIG	EIRNKANGYTYAASVKG
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KABAT V A

CC4	ABLVCPGASVTKLSCSKASGYFFF	SYCPL	WVKCRPGGLEWIG	WVKCRPGGLEWIG
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FIG. 10a

SUBSTITUTE DRAWING

ER 3

CDR 3

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RISITROTTSKNOFFLQLNSVTTEDSTATVYCAR
FISITROTTSKNOFFLQLNSVTTEDSTATVYCA
RISITROTTSKNOFFLQLNSVTTEDSTATVYCA
RISITROTTSKNOFFLQLNSVTTEDSTATVYCA

EGNADGFTAY
DROKLGFTAY
DSSGSMY
VSSGYESMY

```

HGGSSGXFY
NDGYY
LORYAMY
KRDYDXYDROYYAMY
YYDGSSFFAY
EGYYYFAV
IYYDGSSDYYAMY
13 RE.
21 RE.
29 RE.
37 RE.
32 RE.

```

Ps. gene/Unproductive
Unproductive
Unproductive
Unproductive
Unproductive

KADMTDKSSSTAYMLAPLTSEDSAVNYGAP
KADMTDKSSSTAYMLAPLTSEDSAVNYGAP

40 88. Unproductive
22 88. Unproductive

PGTYAHC
YBBMFDY
PNCHYHYYGMDY
LYYYAHCY
SSGVDY
GAAATNAY
GGFAY
SPMZY
EVPGFYATDY
MDYVGGSSLWTFAY
TVVVAFDY
IGDVSFTYFDR
TGTFRAY
24. re.
9. re.
23. re.
15. re.

Ps. gene
Ps. gene/Unproductive
Unproductive
Unproductive
Unproductive

ATTISROMSOCISIVYQWALRAEDSATYYCAG

YMLGAMY
GYYDGSYAMCY
23 82.

Unproductive

RFTISRDNAKTYTLYOMSSLSRSSEDTAVYYCA
RFTISRDNTKTYTLYOMSSLSRSSEDTAVYYCA
RFTISRDNSKTYTLYOMSSLSRSSEDTAVYYCA
RFTISRDNSKTYTLYOMSSLSRSSEDTAVYYCA
RFTISRDNSKTYTLYOMSSLSRSSEDTAVYYCA
RFTISRDNSKTYTLYOMSSLSRSSEDTAVYYCA
RFTISRDNTKTYTLYOMSSLSRSSEDTAVYYCA
RFTISRDNAKTYTLYOMSSLSRSSEDTAVYYCA
RFTISRDNAKTYTLYOMSSLSRSSEDTAVYYCA

AKFHLYFDY
 REGVVERSLDGDV
 RGLHWFDP
 RNYGSSPFDY
 PPMMPSY
 43 nt.
 28 nt.
 35 nt.

Ps.gene
Ps.gene
Ps.gene
Ps.gene
Ps.gene/Unproductive
Ps.gene/Unproductive
Unproductive

RETTISRDOOKSKSRVYLOMNSLRAEDTSIYVCT

3C 85.1

Unproductive

KATIE JACKIE SALLY MEL SPENCER SAM YFC

REBROSSAGE:

FIG. 10 b

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CDR 2

FRAMWORK 3

CDR 3

KABAT HUMAN V81

BACKFQG	RVTIRRHKSTSTAYMELSSLRSED TAVYYCAR	GEGWDHFDY
GYAQKPG	RVTMTRNTSISATAYMELSSLRSED TAVYYCAR	GSRYGYDCSGYYYL
		LAHFSGSPVWDWFDP

KABAT HUMAN V82

KHCLQPSILKS	RVTISVDTSKNQFSLKLSSTAA DTAVYYCAR	GGVVPAAIMDV
KS	RVTISVDTSKNQFSLKLSSTAA DTAVYYCAR	MARYYDFWSGYSAYYDY
SLKS	RLSISCDTSRNQFSLRLSSSTAA DTAVYYCAR	HRNWGSPVHF DY
	ESTSTAYMELSSLRSED TAVYYCAR	DSYGDYCGHY

KABAT HUMAN V83

ISYITSSSSYTNYADSVKG	RFTISRDNAKNSLYLQMNSLRAED TAVYYCAR	DGRFGTYSPSDY
SVKG	RFTISRDDS KSIAYLQVNLSLKD TAVYYCTR	TIYYDSSGYPY W
YADSVKG	RFTISRDNAKNSLF LQMSSLR AEDTAVYYCAR	GIALDAFDI
YYADSVRD	RFTISRDNSKNTLYLQMNSLRAED TAVYYCAK	53 NT. UNPROD REARR
DSVKG	RFTISRDNAKNSLYLQMNSLRAED TAVYYCAR	DHSGTGGGGSGSYF
VSAISGGGGSTYYADSVKG	RFTISRDNPKNTLYLQMNSLRS EDTAVYYCAR	KDNLWFDP
AVISYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAED TAVYYCAR	DLGGRGVVVV PAPGGRSI YYYYGM DV
GAVISYDGSNKYYADSVKG	RFTISRDNSKNTLYLQMNSLRAED TAVYYCAS	LEGIGTI YYYYGM DV
	AKNSLYLQMNSLRAED TAVYYCVR	DDSSSWPKHFOH
QYAA SVKG	RFTISRDDS KNSLYLQMNSLNTED TAVYYCVR	SGVVPYLDY

KNOWN FAMILY

AVYYCAR	DPRIAARPDYYYYMDV
TAMYYCAR	GAEVVEPTARYYYGLNV

FIG. 11

SUPERIMPOSED

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PEI	CDPI	FR2
YTT	SYG1S	WVTTGPWTQJLRWMG
GEKPQSSVKVSCKASGYTFT	DYFMN	WMRQAPGQRLLEWMG
QVQLQEIGPRGEASETSLSLICAVSGDSIS	SGNW-1	WVRQPPGKGLEWIG
QVQLQEESGPGLVK*SETLSLTCTVSGGSIS	SYWWS	WIRQPPGKGLEWIG
GYTT	NYCMH	WVRQDHAQGLEWMG
QVQLQEESGPGLVKPSETLSLYCAVSGDSIS	SGNW-1	WVRQPPGKGLEWIG
GPRLGZASETSLSLTCTVSGGSIS	SSSYYW	WIRQPPGKGLEWIG
QVQLQEESGPGLVKPSETLSLTCTVSGGSIS	SYWWS	WIRQPPGKGLEWIG
LSLICAVSGSSIS	SGNW-1	WVRQPPGKGLEWIG
SETLSLTCAVYGGSFS	GYWWS	WIRQPPGKGLEWIG
QVCLVQSGAEVKKGASVKVSCKASGYTFT	NYCMH	WVRQVLAQGLEWMG
SETLSLICAVSGDSIS	SGNW-1	WVRQPPGKGLEWIG
SRAQTGEASETSLSLTCTVSGGSIS	SSSYWNG	WIRQPPGKGLEWIG
GPICTVSGGSVSSGS	YYWS	WIRQPPGKGLEWIG
GLVKPSETSLSLTCTVSGGSIS	SYWWS	WIRQPPGKGLEWIG
SETLSLICAVSGDSIS	SGNW-1	WVRQPPGKGLEWIG
QVCLVQSGAEVKKGSSVKVSCKASGGTS	SYAIS	WVRQAPGQGLEWMG
QVCLVQSGAGLKPSETSLSLTCAVYGGSFS	GYWWS	WIRQPPGKGLEWIG
QVCLVQSGAGLKPSETLSLTCTVSGGSIS	SSSYWNG	WIRQPPGKGLEWIG
GPICTVSGGSVSSGS	SGGYYWS	WIRQNPQGKGLEWIG

- indicates stop codon (unsure as sequence remains in frame)
- sequence terminates due to internal restriction site
- lower case denotes frame shift

FR2	CDR1
WISAYNGNTNYAQKFCQG	RVTIMTDTSTSTAYMELRSLRSDDTAVYYCAR
WINAGNGNTKYSQKLCQG	RVTITRDTSASTAYMQLSSLRSEDATAVYYCAR
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLLSS.
RIYTSGSTNYNPSLKS	RVTISVDTSKNQFSLKLLSSVTAADTAVYYCAR
LVCPSDGSTSAYQKFQAA	RVTITRDTSMSTAYMELSSLRSEDATAMYYCAR
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLLSS.
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLLSS.
YIYYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLLSS.
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLLSS.
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLLSS.
EIHHSGSTNYNPSLKS	RVTITRDTSMSTAYMELSSLRSEDATAMYYCAR
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLLSS.
SIYYGSTYYNPSLKS	RVTIPVDTSKNQFSLKLLSS.
YIYYSGSTNYNPSLKS	RVTISVDTSKNQFSLKLLSSVTAADTAVYYCAR
RIYTSGSTNYNPSLKS	RITMSVDTSKNQFYLKLLSS.
EIHHSGSTYYNPSLKS	RITMSVDTSKNQFYLKLLSS.
RIIPILGANYAQKFCQG	RVTITADKSTSTAYMELSSLRSEDATAVYYCAR
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLLSS.
EIHHSGSTNYNPSLKS	RVTISVDTSKNQFSLKLLSS.
YIYYSGSTYYNPSLKS	RVTISVDTSKNQFSLKLLSSVTAADTAVYYCAR

FIG. 12

RESTITUTIONS

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PSWL

HindIII site AAGCTT

M K Y L L P T A A
GCATGCAAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G I I I L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCAACAGCGATGGCCCAGGTGCAGGTGCAGGGAGTC
70 80 90 100 110 120

G P G I V A P S Q S L S I T C T V S G F
GGACCTGGCTGGGGGCGCTACAGAGCGTGTCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGCTATGGTGTAACTGGGTTGCCAGGCTCCAGGAAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGGTGTGGAAACACAGACTATAATTCACTGCTCTCAAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCCAGGCCAAGTTTCTTAAATGAAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTACTGGGC
370 380 390 400 410 420

Q G T T V T V S S SmaI
CAAGGCACCAACGGTCACCGCTCTCTCTATAATAAGAGCTATGGGGCTAAGCTCGAATT
430 440 450 460 470 480

FIG. 13

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HindIII AAGCTT

M K Y L L P T A A
 GCATGCAAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
 10 20 30 40 50 60

A G L L L A A C P A M A Q V Q L Q E S
 GCTGGATTGTTATTACTCGCTGCCAACGCGATGGCCAGGTGCAGCTGCAGGAGTC
 70 80 90 100 110 120

G P G L V A P S Q S I S I T C T V S G F
 GGACCTGGCTGGTGGCGCCCTCACAGAGCCTGTCATCACATGCACCGCTCTCAGGGTTC
 130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
 TCATTAACGGCTATGGTAACTGGTTGGCAGGAAAGGGTCTGGAGTGG
 190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
 CTGGAAATTTGGGTGATGAAACAGAGACTATAATTGAGCTCTCAAATCCAGACTG
 250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
 AGCATGAAAGGACAACCTCAAGAGGCGAGTTTTCTAAAAATGAACAGTCTGCACACT
 310 320 330 340 350 360

C D T A R Y Y C A R E R D Y R L D Y W G
 GATGAGAGCCAGGTACTCTGCGAGAGAGAGATTATAGGCTTGACTACTGGGC
 370 380 390 400 410 420

Q G T T V T V S S
 CAAGGAAACCGCTACCGCTCTCTCATATAAGAGCTCGAATTGCCAAGCTTGCATGC
 430 440 450 460 470 480

M K Y L L P T A A A G
 AAAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGGA
 490 500 510 520 530 540

L L L L A A Q P A M A D I V L T Q S P A
 TTGTTATTACTCGCTGCCAACCGCGATGGCCGACATCGTCTGACTCAGTCTCCAGCC
 550 560 570 580 590 600

S L S A S V G E T V T I T C R A A S G N I
 TCCCTTCTCGCTGTGGAGAAACTGTCAACCATCACATGTCAGCAAGTGGGAATATT
 610 620 630 640 650 660

H N Y L A W Y Q Q K Q G K S P Q L L V Y
 CACAATTATAGCATGGTATGCGAGAAACAGGGAAAATCTCTGAGCTCTGGTCTAT
 670 680 690 700 710 720

FIG. 14a

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Y T T T L A D G V P S R F S G S G S G T
TATACAACAAACCTTACGAGATGGTGTGCCATCAAGGTTAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

Q Y S L K I N S L Q P E D F G S Y Y C Q
CAATATTCTCTCAAGATCAACAGCCTGCACCTGAAGATTGGGAGTTATTACTGTCAA
790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
CATTTGGAGTACTCCTCGGACGTTGGAGGCAAGCTGGAAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATT
910

FIG. 14 b

pSWIHPOLIMYC

HindIII site AAGCTT

M K Y L L P T A A
GCATGGCAAACTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
GCTGGATTGGTATTACTCGTGCCTAACCAACCAGCGATGCCAGGTGCAGCTGCAG
70 80 90 100 110 PstI

Polylinker
TCTAGA GTCGAC CTCGAG
XbaI Sall XhoI

MYC PEPTIDE
V T V S S E O K L I S E E D L N * *
GGTCACCGTCTCCTCAGAACAAAAACTCATCTCAGAAGAGGATCTGAATTAATAA
BstEII

GGGCTAAGCTCGAATT

FIG. 15

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1
VH3 QVQLQESGPVELVKPGASVKMSCKASGYTFT
VH8 QVQLQESGPVELVKPGASVKMSCKASGYTFT
VH-D1.3 QVQLKESGPGLVAPSQSLSITCTVSGFSLT

50 CDR2
VH3 YINPYNDGTYNEKFKG
VH8 YINPYNDGSKYNEKFKG
VH-D1.3 MIW GDGNTDYNALKS

95 CDR3
VH3 LLLRYFFDY
VH8 GAVVSYYAMDY
VH-D1.3 ERDYRLDY

CDR1
SYVMH
SYVMH
GYGVN

49
WVKQKPGAGLEWIG
WVKQKPGQGLEWIG
WVRQPPGKGLEWLG

94
KATLTSDKSSSTAYMELSSLTSEDSAVYYCAV
KATLTADKSSNTAYMOLSSLTSEDSAVYYCAR
RLSISKDNSKSQVFLKMNSLHTDDTARYYCAR

113
WGQGTTVTVSS
WGQGTTVTVSS
WGQGTTTVSS

FIG. 16

FR1 QVQLQESGGGLVQPGGSLRLSCAASGFTFS
SYAMS CDR1

FR2 WVRQAPGKGLEWVS

AISGGSTYYADSVKG CDR2

FR3 RFTISRDNSKNTLYLQMNSLRAEDTAVYYCAM
WRGIATPVSFDLGYFDY CDR3

FIG. 17

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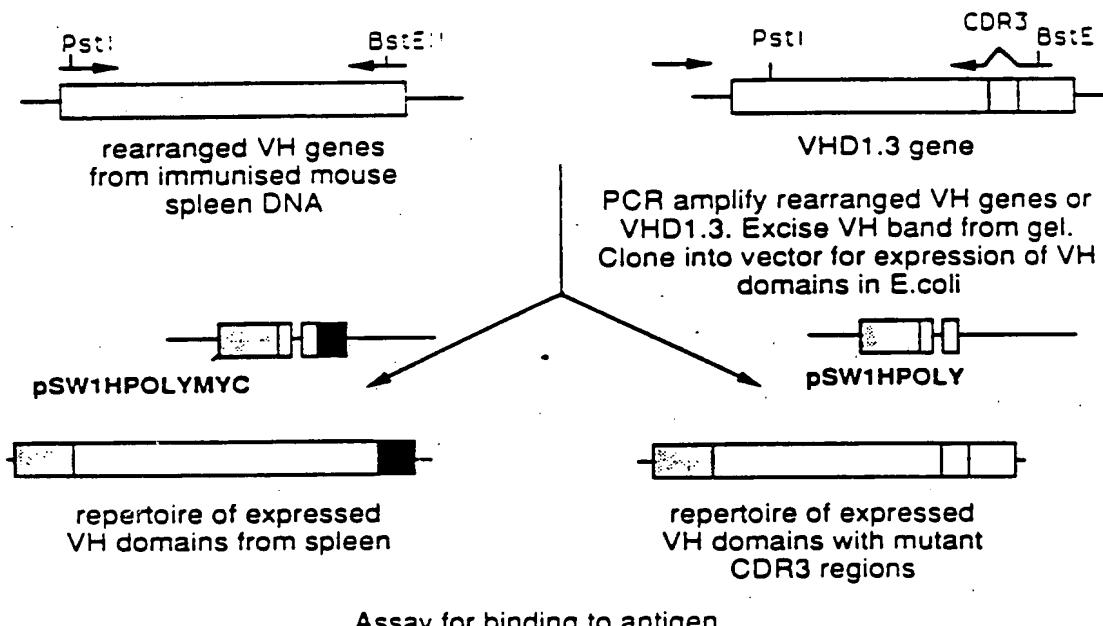


FIG. 18

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PSW24PCLV

HindIII AAGCTT

M K Y I I P T A A
GCATGCAAAATTCTATTTCAGGAGACAGTCATAATGAAATACCTATTGCCATACGGAGCC
10 20 30 40 50 60

A G L L L L A A Q P A M A Q V Q L Q
GCTGGATTGTTATTACTCGCTGCCAACCGAGCGATGGCCAGGTGCAGCTGCAG
70 80 90 100 110 PstI

TCTAGA GTCGAC CTCGAG
XbaI SalI XhoI

V T V S S
GGTCACCGCTCTCTCTATAATAAGAGCTCGAATTGCCAAGCTTGCATGC
BstEII 430 440 450 460 470 480

M K Y I I P T A A A G
AAATTCTATTTCAGGAGACAGTCATAATGAAATACCTATTGCCATACGGCAGCCGCTGGA
490 500 510 520 530 540

I I I I A A Q P A M A D I V L T Q S P A
TTGTTATTACTCGCTGCCAACCGAGCGATGGCCAGATCGTCTGACTCAGTCAGCTCCAGCC
550 560 570 580 590 600

S I S A S V G E T V T I T C R A S G N I
TCCCTTTCTGCTCTGGGAGAAACTGTCACCATCACATGTCAGCAAGTGGGAATATT
610 620 630 640 650 660

H N Y I A W Y Q Q K Q G K S P O L L V Y
CACATTAACTGATGGTATCAGCAGAAACAGGGAAATCTGCTCAGCTCCTGGTCTAT
670 680 690 700 710 720

Y T T I A D G V P S R F S G S G S G T
TATACAACAAACCTTACGCAGATGGTGTGCCATCAAGGTTCAAGTGGCAGTGGATCAGGAACA
730 740 750 760 770 780

Q Y S L N I N S L Q P E D F G S X Y C Q
CAATATTCTCTCAAGATCAACAGCCTGCAACCTGAAGATTTGGAGTTATTACTGTCAA
790 800 810 820 830 840

H F W S T P R T F G G G T K L E I K R
CATTTTGGAGTACTCTCGGACGTTCGGTGGAGGCACCAAGCTGGAAATCAAACGGTAA
850 860 870 880 890 900

TAAGAGCTCGAATTG
910

FIG. 19

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FIG. 20

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M K Y L L P T A A
GCATGCAAATTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTTATTACTCGCTGCCAACAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGCGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAAACTGGGTTGCCAGCCTCCAGGAAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGTGATGGAAACACAGACTATAATTAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCAAGAGCCAAAGTTCTTAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAGATTATAGGCTTGACTIONGGGC
370 380 390 400 410 420

Q G T T V T V S S R T P E M P V L E N R
CAAGGCACACGGTCACCGTCTCCTCACGGACACCAGAAATGCCTGTTCTGGAAAACCGG
430 440 450 460 470 480

A A Q G D I T A P G G A R R L T G D Q T
GCTGCTCAGGGCGATATTACTGCACCCGGCGGTGCTCGCCGTTAACGGGTGATCAGACT
490 500 510 520 530 540

A A L R D S L S D K P A K N I I L L I G
GCCGCTCTGCGTATTCTCTAGCGATAAACCTGCAAAAATATTATTTGCTGATTGGC
550 560 570 580 590 600

D G M G D S E I T A A R N Y A E G A G G
GATGGGATGGGGACTCGGAAATTACTGCCGCACGTAAATTATGCCGAAGGTGCGGGCGC
610 620 630 640 650 660

F F K G I D A L P L T G Q Y T H Y A L N
TTTTTAAAGGTATAGATGCCTACCGCTTACCGGGCAATACACTCACTATGCGCTGAAT
670 680 690 700 710 720

K K T G K P D Y V T D S A A S A T A W S
AAAAAAACCGGAAACCGGACTACGTCAACCGACTCGGCTGCATCAGCAACCGCCTGGTCA
730 740 750 760 770 780

FIG. 21a

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T G V K T Y N G A L G V D I H E K D H P
ACCGGTGTCAAAACCTATAACGGCGCGTGGCGTCGATATTACGAAAAAGATACCCA
790 800 810 820 830 840

T I L E M A K A A G L A T G N V S T A E
ACGATTCTGGAAATGGCAAAAGCCGCAGGTCTGGCGACCGTAACGTTCTACCGCAGAG
850 860 870 880 890 900

L Q D A T P A A L V A H V T S R K C Y G
TTGCAGGATGCCACGCCGCTGCGCTGGCACATGTGACCTCGCGAAATGCTACGGT
910 920 930 940 950 960

P S A T S E K C P G N A L E K G G K G S
CCGAGCGCGACCAGTGA AAAATGTCCGGTAACGCTCTGGAAAAAGGCCGAAAGGATCG
970 980 990 1000 1010 1020

I T E Q L L N A R A D V T L G G G A K T
ATTACCGAACAGCTGCTTAACGCTCGCCGACGTTACGCTGGCGGGCGCAAAACC
1030 1040 1050 1060 1070 1080

F A E T A T A G E W Q G K T L R E Q A Q
TTTGCTGAAACGGCAACCGCTGGTGAATGGCAGGGAAAACGCTGCGTGAACAGGCACAG
1090 1100 1110 1120 1130 1140

A R G Y Q L V S D A A S L N S V T E A N
GCGCGTGGTTATCAGTTGGTGAGCGATGCTGCCTCACTGAATTGGTACGGAAGCGAAT
1150 1160 1170 1180 1190 1200

Q Q K P L L G L F A D G N M P V R W L G
CAGCAAAAACCCCTGCTGGCTGTTGCTGACGGCAATATGCCAGTGGCTGGCTAGGA
1210 1220 1230 1240 1250 1260

P K A T Y H G N I D K P A V T C T P N P
CCGAAAGCAACGTACCATGGCAATATCGATAAGCCCGCAGTCACCTGTACGCCAAATCCG
1270 1280 1290 1300 1310 1320

Q R N D S V P T L A Q M T D K A I E L L
CAACGTAATGACAGTGTACCAACCCCTGGCGCAGATGACCGACAAAGCCATTGAATTGTTG
1330 1340 1350 1360 1370 1380

S K N F K G F F L Q V E G A S I D K Q D
AGTAAAATGAGAAAGGCTTTCTCTGCAAGTTGAAGGTGCGTCAATCGATAAACAGGAT
1390 1400 1410 1420 1430 1440

H A A N P C G Q I G E T V D L D E A V Q
CATGCTGCGAATCCTTGTGGCAAATTGGCGAGACGGTCGATCTCGATGAAGCCGTACAA
1450 1460 1470 1480 1490 1500

P A L E F A K K E G N T L V I V T A D H
CGGGCGCTGGAATTGCTAAAAGGAGGGTAACACGCTGGTCATAGTCACCGCTGATCAC
1510 1520 1530 1540 1550 1560

FIG. 21b

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A H A S Q I V A P D T K A P G L T Q A L
GCCACGCCAGCCAGATTGTTGCCGGATACCAAAGCTCCGGGCCTCACCCAGGCGCTA
1570 1580 1590 1600 1610 1620

N T K D G A V M V M S Y G N S E E D S Q
AATACCAAGATGGCGCAGTGTGATGGTGTAGTTACGGGAACCTCCGAAGAGGATTACAA
1630 1640 1650 1660 1670 1680

E H T G S Q L R I A A Y G P H A A A N V V
GAACATACCGGSCAGTCAGTTGGTATTGGCGGTATGGCCCGATGCCGCCAATGTTGTT
1690 1700 1710 1720 1730 1740

G L T D Q T D L F Y T M K A A L G L K *
GGACTGACCGACCAAGACCGATCTCTACACCATGAAAGCCGCTCTGGGCTGAAATAA
1750 1760 1770 1780 1790 1800

AACCGCGCCCGGGAGTGAATTTCGCTGCCGGGTGGTTTTTGCTGTTAGC
1810 1820 1830 1840 1850

FIG. 21c

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M K Y L L P T A A
GCATGCAAATTCTATTCAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCC
10 20 30 40 50 60

A G L L L A A Q P A M A Q V Q L Q E S
GCTGGATTGTATTACTCGCTGCCAACAGCGATGGCCAGGTGCAGCTGCAGGAGTCA
70 80 90 100 110 120

G P G L V A P S Q S L S I T C T V S G F
GGACCTGGCCTGGTGGGCCCTCACAGAGCCTGTCCATCACATGCACCGTCTCAGGGTTC
130 140 150 160 170 180

S L T G Y G V N W V R Q P P G K G L E W
TCATTAACCGGCTATGGTGTAAACTGGGTTGCCAGCCTCCAGGAAGGGTCTGGAGTGG
190 200 210 220 230 240

L G M I W G D G N T D Y N S A L K S R L
CTGGGAATGATTTGGGTGATGGAAACACAGACTATAATTCAAGCTCTCAAATCCAGACTG
250 260 270 280 290 300

S I S K D N S K S Q V F L K M N S L H T
AGCATCAGCAAGGACAACCTCAAGAGCCAAGTTTCTTAAATGAACAGTCTGCACACT
310 320 330 340 350 360

D D T A R Y Y C A R E R D Y R L D Y W G
GATGACACAGCCAGGTACTACTGTGCCAGAGAGAGATATAGGCTTACTACTGGGGC
370 380 390 400 410 420

Q G T T V T V S S * *
CAAGGCACCAAGGTACCGTCTCCTCATAATAAGAGCTATCCGGAGCTTGCATGAAA
430 440 450 460 470 480

M K Y L L P T A A A G L
TTCTATTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTG
490 500 510 520 530 540

L L L A A Q P A M A D I E L V D L E I K
TTATTACTCGCTGCCAACAGCGATGGCCAGCATCGAGCTCGACCTCGAGATCAAA
550 560 570 580 590 600

R E Q K L I S E E D L N * *
CGGGAACAAAACATCTAGAAGAGGATCTGAATTAAATGATCAAACGGTAATAAG
610 620 630 640 650 660

GATCCAGCTCGAATTG
670

FIG. 22

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Q V Q L Q E S G P G L V Q P S Q S L S I
CAGGTGCAGCTGCAGGAGTCAGGACCTGGCTAGTGCAGCCCTCACAGAGCCTGTCCATC

10 20 30 40 50 60

T C T V S G F S L T S Y G V H W V R Q S P
ACCTGCACAGTCTCTGGTTCTATTAACTAGCTATGGTGTACACTGGGTTGCCAGTCT
C 70 80 90 100 110 120

P G K G L E W L G M I W G D G N T D Y N
CCAGGAAAGGTCTGGAGTGGCTGGGAATGATTGGGTGATGAAACACAGACTATAAT
130 140 150 160 170 180

S A L K S R L S I S K D N S K S Q V F L
TCAGCTCTCAAATCAGACTGAGCATCAGCAAGGACAACCTCAAGAGCCAAGTTTCTTA
190 200 210 220 230 240

K M N S I H T D D T A R Y Y C A R E R D
AAAATGAACAGTCTGCACACTGATGACACAGCCAGGTACTACTGTGCCAGAGAGAGAT
250 260 270 280 290 300

Y R L D Y W G Q G T T V T V S S
TATAGGCTTGACTACTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA
310 320 330 340

FIG. 23

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